

10/019114

SEQUENCE LISTING

10 Reg'd PCT 20 MAY 2004

<110> Seishi KATO

Tomoko KIMURA

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 1997.13000

<140> US 10/019,114

<141> 2000-06-16

<150> JP 11-188835

<151> 1999-07-02

<160> 30

<210> 1

<211> 233

<212> PRT

<213> Homo sapiens

<400> 1

Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu Leu Leu Gly Ser

1 5 10 15

Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn Pro Glu Ala Asn

20 25 30

Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr Pro Tyr Glu Glu

35 40 45

Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly Ile Tyr Arg Ile

50 55 60

Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro Lys Pro Ala Val
65 70 75 80

Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn Trp Ile Cys Asn
85 90 95

Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp Ser Gly Tyr Asp
100 105 110

Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Leu
115 120 125

Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe Ser Leu Asp Glu
130 135 140

Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe Ile Ile Glu Lys
145 150 155 160

Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser Gln Gly Thr Thr
165 170 175

Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu Ala Lys Lys Ile
180 185 190

Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val Lys Tyr Thr Gln
195 200 205

Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg Val Val Lys Val
210 215 220

Cys Asp Phe Pro Ser Phe Asn Leu Lys
225 230

<210> 2

<211> 273

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala

1 5 10 15

Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala

 20 25 30

Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val

 35 40 45

Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr

 50 55 60

Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala

 65 70 75 80

Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser

 85 90 95

Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg

 100 105 110

Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly

 115 120 125

Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg

 130 135 140

Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp

 145 150 155 160

Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys

 165 170 175

Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val

 180 185 190

Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp

 195 200 205

Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu

 210 215 220

Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu

 225 230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln

245 250 255
Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
260 265 270
Ser
<210> 3
<211> 282
<212> PRT
<213> Homo sapiens

<400> 3
Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu
1 5 10 15
Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro
20 25 30
Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu
35 40 45
Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser His Thr Leu Thr
50 55 60
Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys
65 70 75 80
Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp
85 90 95
Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala
100 105 110
Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys
115 120 125
Arg Ser Glu Asn Lys Asn Glu Gly Gln Asp Ala Thr Met Tyr Cys Lys
130 135 140
Ser Val Gly Tyr Pro His Pro Asp Trp Ile Trp Arg Lys Lys Glu Asn
145 150 155 160

Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe Ile Ile
165 170 175
Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln Ile Thr
180 185 190
Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile Gly Ser
195 200 205
Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala Pro Leu
210 215 220
Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Leu Val Val Ile
225 230 235 240
Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro Asp Asp
245 250 255
Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn His Lys
260 265 270
Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn
275 280

<210> 4

<211> 238

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Leu Asn Glu His Ser Met Gln Ala Leu Ser Trp Arg Lys Leu
1 5 10 15
Tyr Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu
20 25 30
Leu Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala
35 40 45
Asp His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr
50 55 60

Thr Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys
65 70 75 80

Ile Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser
85 90 95

Val Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala
100 105 110

Trp Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val
115 120 125

Val Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly
130 135 140

Gln Pro Arg Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn
145 150 155 160

Val Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser
165 170 175

Thr Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Val
180 185 190

His Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln
195 200 205

Glu Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp
210 215 220

His Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala
225 230 235

<210> 5

<211> 372

<212> PRT

<213> Homo sapiens

<400> 5

Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro

1 5 10 15
Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val
20 25 30
Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu
35 40 45
Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu
50 55 60
Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser
65 70 75 80
Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr
85 90 95
Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu
100 105 110
Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg
115 120 125
Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly
130 135 140
Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His
145 150 155 160
Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe
165 170 175
Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val
180 185 190
Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val
195 200 205
Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr
210 215 220
Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu
225 230 235 240
Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val

245 250 255
Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg
260 265 270
Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala
275 280 285
Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe
290 295 300
Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser
305 310 315 320
Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala
325 330 335
Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu
340 345 350
Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln
355 360 365
Asp Ser Ala Leu
370

<210> 6
<211> 146
<212> PRT
<213> Homo sapiens

<400> 6
Met Trp Lys Leu Trp Arg Ala Glu Glu Gly Ala Ala Leu Gly Gly
1 5 10 15
Ala Leu Phe Leu Leu Phe Ala Leu Gly Val Arg Gln Leu Leu Lys
20 25 30
Gln Arg Arg Pro Met Gly Phe Pro Pro Gly Pro Pro Gly Leu Pro Phe
35 40 45

Ile Gly Asn Ile Tyr Ser Leu Ala Ala Ser Ser Glu Leu Pro His Val
50 55 60
Tyr Met Arg Lys Gln Ser Gln Val Tyr Gly Glu Val Gln Pro Arg Arg
65 70 75 80
Ala Pro Gly Arg Glu Gly Arg Gln Ala Gly Pro Gly Trp Pro Gly Pro
85 90 95
Ser Trp Leu Asp Leu Trp Pro Pro Leu Gly Arg Leu Val Gly Thr Ser
100 105 110
Pro Cys Ala Gly Cys Pro Leu Arg Asp Thr Arg Phe Pro Gly Leu Glu
115 120 125
Gly Arg Ser Pro Arg Arg Arg Ala Pro Leu Gln Gly Glu Pro Arg Pro
130 135 140
Cys Arg
145

<210> 7
<211> 302
<212> PRT
<213> Homo sapiens

<400> 7
Met Lys Ala Pro Gly Arg Leu Val Leu Ile Ile Leu Cys Ser Val Val
1 5 10 15
Phe Ser Ala Val Tyr Ile Leu Leu Cys Cys Trp Ala Gly Leu Pro Leu
20 25 30
Cys Leu Ala Thr Cys Leu Asp His His Phe Pro Thr Gly Ser Arg Pro
35 40 45
Thr Val Pro Gly Pro Leu His Phe Ser Gly Tyr Ser Ser Val Pro Asp
50 55 60
Gly Lys Pro Leu Val Arg Glu Pro Cys Arg Ser Cys Ala Val Val Ser

65 70 75 80
Ser Ser Gly Gln Met Leu Gly Ser Gly Leu Gly Ala Glu Ile Asp Ser
 85 90 95
Ala Glu Cys Val Phe Arg Met Asn Gln Ala Pro Thr Val Gly Phe Glu
 100 105 110
Ala Asp Val Gly Gln Arg Ser Thr Leu Arg Val Val Ser His Thr Ser
 115 120 125
Val Pro Leu Leu Leu Arg Asn Tyr Ser His Tyr Phe Gln Lys Ala Arg
 130 135 140
Asp Thr Leu Tyr Met Val Trp Gly Gln Gly Arg His Met Asp Arg Val
145 150 155 160
Leu Gly Gly Arg Thr Tyr Arg Thr Leu Leu Gln Leu Thr Arg Met Tyr
 165 170 175
Pro Gly Leu Gln Val Tyr Thr Phe Thr Glu Arg Met Met Ala Tyr Cys
 180 185 190
Asp Gln Ile Phe Gln Asp Glu Thr Gly Lys Asn Arg Arg Gln Ser Gly
 195 200 205
Ser Phe Leu Ser Thr Gly Trp Phe Thr Met Ile Leu Ala Leu Glu Leu
 210 215 220
Cys Glu Glu Ile Val Val Tyr Gly Met Val Ser Asp Ser Tyr Cys Arg
225 230 235 240
Glu Lys Ser His Pro Ser Val Pro Tyr His Tyr Phe Glu Lys Gly Arg
 245 250 255
Leu Asp Glu Cys Gln Met Tyr Leu Ala His Glu Gln Ala Pro Arg Ser
 260 265 270
Ala His Arg Phe Ile Thr Glu Lys Ala Val Phe Ser Arg Trp Ala Lys
 275 280 285
Lys Arg Pro Ile Val Phe Ala His Pro Ser Trp Arg Thr Glu
 290 295 300

<210> 8

<211> 194

<212> PRT

<213> Homo sapiens

<400> 8

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu

1 5 10 15

Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp

20 25 30

Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr

35 40 45

Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr

50 55 60

Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys

65 70 75 80

Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly

85 90 95

Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp

100 105 110

Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser

115 120 125

Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg

130 135 140

Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala

145 150 155 160

Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys

165 170 175

Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His

180 185 190

Gly Phe

<210> 9

<211> 542

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe
1 5 10 15
Leu Ser Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser
20 25 30
Tyr Ser Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn
35 40 45
Trp Ala Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser
50 55 60
Val Asn Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn
65 70 75 80
Ile Val Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His
85 90 95
Asn Thr Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr
100 105 110
Thr Glu Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg
115 120 125
Lys Leu Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr
130 135 140
Leu Gly Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro
145 150 155 160
Arg Gln Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu
165 170 175

Gln Glu Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala
180 185 190
Arg Ala Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu
195 200 205
Lys Ala Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg
210 215 220
Cys Asn Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser
225 230 235 240
Lys Ser Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu
245 250 255
Ser Val Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr
260 265 270
Val Trp Ser Arg Val Val Val Thr Glu Ile Ser Tyr Met Arg His Val
275 280 285
Cys Ile Val Asn Ile Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe
290 295 300
Ile Ile Gly Ser His Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys
305 310 315 320
Val Ala Val Thr Phe Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe
325 330 335
Trp Met Leu Phe Lys Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile
340 345 350
Phe Arg Arg Met Met Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile
355 360 365
Gly Tyr Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr
370 375 380
Glu Pro Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp
385 390 395 400
Asp Asn Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile
405 410 415

Val Ala Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln
420 425 430

Arg Pro Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met
435 440 445

Arg Ile Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr
450 455 460

Trp Gly Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe
465 470 475 480

His Ile Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu
485 490 495

Leu Phe Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met
500 505 510

Arg Met Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser
515 520 525

Leu Gly Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly
530 535 540

<210> 10

<211> 276

<212> PRT

<213> Homo sapiens

<400> 10

Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu
1 5 10 15

Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro
20 25 30

Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala
35 40 45

Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala

50 55 60
Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser
65 70 75 80
Arg Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro
85 90 95
Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp
100 105 110
Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val
115 120 125
Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn
130 135 140
Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met
145 150 155 160
Asp Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile
165 170 175
Thr Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly
180 185 190
Arg Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu
195 200 205
Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe
210 215 220
Ser Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly
225 230 235 240
Ser Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu
245 250 255
Ala Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro
260 265 270
Ser Leu Ser Pro
275

<210> 11
<211> 699
<212> DNA
<213> Homo sapiens

<400> 11

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gacaagaaag gaaacaatgc aaaccctgaa gctaataatga atattagcca gattatttct	120
tactgggtt atccttatga agagtatgtat gttacaacaa aagatggta taticcttgaa	180
atttatagga ttcccacatgg aagaggatgc ccagggagga cagctccaaa gcctgctgtg	240
tatggcagc atggcttaat tgcatctgcc agtaactgga tttgcaacct gcccaacaac	300
agtttggctt tccttctggc agatagtggt tatgacgtgt ggttgggaa cagccgagga	360
aacacttggt ccagaaaaca ccttaaatttgc tcaccgaaat caccagaata ctgggccttc	420
agtttggatg agatggctaa atatgacctt ccagccacaa tcaattttat catagagaaa	480
actggacaga agcgactcta ctacgtggc cactcacaag gcaccaccat agctttata	540
gcattttcta caaacccaga actggctaaa aagattaaga tatttttgc actggctcca	600
gttgtcacag ttaaatacac ccaaagtccct atgaaaaaac taacaaccct ttccaggcga	660
gttagttaagg tatgtgactt cccaaaggaaaaatctgaaa	699

<210> 12
<211> 819
<212> DNA
<213> Homo sapiens

<400> 12

atgaggggct ctcaggaggt gctgctgatg tggcttcgg tggatggcagt gggccggcaca	60
gagcacgcct accggcccgg ccgtagggtg tgtgctgtcc gggctcacgg ggaccctgtc	120
tccgagtcgt tcgtgcagcg tgtgtaccag cccttcctca ccacctgcga cgggcaccgg	180
gcctgcagca cctaccgaac catctataagg accgcctacc gccgcagccc tgggctggcc	240
cctgccaggc ctcgctacgc gtgctgcccc ggctggaaga ggaccagcgg gtttcctggg	300
gcctgtggag cagcaatatg ccagccgcca tgccggaacg gagggagctg tgtccagcct	360

ggccgctgcc gctgccctgc aggatggcgg ggtgacactt gccagtcaga tgtggatgaa 420
tgcagtgcta ggagggcgg ctgtccccag cgctgcgtca acaccgcccgg cagttactgg 480
tgccagtgtt gggagggca cagctgtct gcagacgta cactctgtgt gcccaaggga 540
gggcccccca gggtgtcccc caacccgaca ggagtggaca gtcaatgaa ggaagaagtg 600
cagaggctgc agtccaggtt ggacctgctg gaggagaagc tgcaagctggt gctggcccca 660
ctgcacagcc tggcctcgca ggcactggag catggctcc cggaccccg cagcctcctg 720
gtgcactcct tccagcagct cggccgcatc gactccctga gcgagcagat ttcccttcctg 780
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<210> 13

<211> 846

<212> DNA

<213> Homo sapiens

<400> 13

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ctcctccag ggccaggcgc cgctcagaac gagccaagga ttgtcaccag tgaagaggtc 120
attattcgag acagccctgt tctccctgtc accctgcagt gtaacctcac ctccagctct 180
cacaccctta catacagcta ctggacaaag aatgggttgg aactgagtgc cactcgtaag 240
aatgccagca acatggagta caggatcaat aagccgagag ctgaggattc aggcgaatac 300
cactgcgtat atcactttgt cagcgtcct aaagcaaacg ccaccattga agtcaaagcc 360
gctcctgaca tcactggcca taaacggagt gagaacaaga atgaaggca ggatgccact 420
atgtattgca agtcagttgg ctaccccac ccagactgga tatggcgcaa gaaggagaac 480
ggatgcccata tggacattgt caataccctt ggccgcttct tcattatcaa caaggaaaat 540
tacactgagt tgaacattgt gaacctgcag atcacggaaag accctggcga gtatgaatgt 600
aatgccacca acgccattgg ctccgcctct gttgtcactg tcctcagggt gcggagccac 660
ctggcccccac tctggccttt ctggaaatt ctggctgaaa ttatcatcct tgtggtgatc 720
attgttgtgt atgagaagag gaagaggcca gatgaggttc ctgacgatga tgaaccagct 780
ggaccaatga aaaccaactc taccaacaat cacaaagata aaaacttgcg ccagagaaac 840
acaaat 846

<210> 14
<211> 714
<212> DNA
<213> Homo sapiens

<400> 14

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gccaaagctta aagcctccag ccggacacctg gctctgctct ccggcttcgc catggtggca	120
atggtggagg tgcagctgga cgctgaccac gactaccac cggggctgct catgccttc	180
agtgcctgca ccacagtgtt ggtggctgtg cacctgtttg cgctcatgtat cagcacctgc	240
atcctgcccc acatcgaggc ggtgagcaac gtgcacaatc tcaactcggt caaggagtcc	300
ccccatgagc gcatgcaccc ccacatcgag ctggcctggg ccttctccac cgtcatcgcc	360
acgctgctct tcctagctga ggtggtgctg ctctgctggg tcaagttctt gcccctcaag	420
aagcagccag gccagccaag gcccaccagc aagccccccg ccagtggcgcc agcagccaac	480
gtcagcacca gcggcatcac cccggggccag gcagctgcca tcgcctcgac caccatcatg	540
gtgcccttcg gcctgatctt tatcgcttc gccgtccact tctaccgctc actggtagc	600
cataagaccc accgacagtt ccaggagctc aacgagctgg cggagtttgc ccgcttacag	660
gaccagctgg accacagagg ggaccacccc ctgacgcccc gcagccacta tgcc	714

<210> 15
<211> 1116
<212> DNA
<213> Homo sapiens

<400> 15

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gcgcctagccc tctgggtctt cctgcgcgcg ctgcgcgtgc actcgggttgt gagcgtgtac	180
atgtgttaacc tggcggccag cgacacctgctc ttccaccctct cgctgcccgt tcgtctctcc	240
tactacgcac tgcaccactg gcccttcccc gacccctgtt gccagacgac gggcgccatc	300

ttccagatga acatgtacgg cagctgcata ttcctgatgc tcatcaacgt ggaccgctac	360
gccgccatcg tgcacccgct gcgactgcgc cacctgcggc ggccccgctg ggcgccgctg	420
ctctgcctgg gcgtgtggc gtcatcctg gtgttgcg tgcccgcgc ccgcgtgcac	480
aggccctcgc gttgccgcta ccgggaccc gaggtgcgcc tatgcttcga gagcttcagc	540
gacgagctgt ggaaaggcag gctgctgccc ctgcgtgc tggccgagggc gctgggcttc	600
ctgctgcccc tggccggcgtt ggtctactcg tcggccgag tcttctggac gctggccgc	660
cccgacgcca cgcagagcca gcggccgggg aagaccgtgc gcctcctgct ggctaacctc	720
gtcatcttcc tgctgtgctt cgtgccctac aacagcacgc tggccgtcta cgggctgctg	780
cggagcaagc tggtggccggc cagcgtgcct gcccgcatc gcgtgcgcgg ggtgctgatg	840
gtgatggtgc tgctggccgg cgccaaactgc gtgctggacc cgctggtgta ctacttttagc	900
gccgaggggct tccgcaacac cctgcgcggc ctggcactc cgccaccgggc caggacctcg	960
gccaccaacg ggacgcgggc ggcgctcgcg caatccgaaa ggtccggcgt caccaccgac	1020
gccaccaggc cggatgccgc cagtcagggg ctgctccgac cctccgactc ccactctctg	1080
tttccattca cacagtgtcc ccaggattcc gccctc	1116

<210> 16

<211> 438

<212> DNA

<213> Homo sapiens

<400> 16

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ccggggccgc cggggctgcc atttatcgac aacatctatt ccctggcagc ctcatccag	180
cttccccatg tctacatgag aaagcagagc caggtgtacg gagaggtaca gccccgacgg	240
gccccggca gggagggccg ccaggctggc ccgggctggc cagggccttc ctggttggac	300
ttatggccgc ccctggcccg actagtcggg acctctccgt gtgccggctg ccctttgagg	360
gacacccgct tcccggtct ggaagggaga agtcctcgac gccgtgcccc cttgcagggg	420
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<210> 17

<211> 906

<212> DNA

<213> Homo sapiens

<400> 17

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cagaaggccc gagacacgct ctacatggtg tggggccagg gcaggcacat ggaccgggtg	480
ctcggcggcc gcacacctaccg cacgctgctg cagctcacca ggatgtaccc cggcctgcag	540
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ggcaagaacc ggaggcagtc gggctccttc ctcagcaccc gctggttcac catgatcctc	660
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cagatgtacc tggcacacga gcaggcgccc cgaagcgccc accgcttcat cactgagaag	840
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<210> 18

<211> 582

<212> DNA

<213> Homo sapiens

<400> 18

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ggaagacgtc acggcctgaa ctactgtgga gttcgtgtt ctgaaaggct ggctgaaata	180

gacatgccat acctcctgaa atatcaaccc atgatgaaaa ccattggcca aaagtactgc 240
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gtcaacatgg gcgataggac tagcatggtg caggaccctg gctctcaagc tcccacatcc 360
tggattagtg agtctcaggt ttcccagaca actgaagttc tgactactag aatcaaagaa 420
atccagagga gtttccaac ctggaccctt gaccagtacc tgagaggtagg actctgtgcc 480
tacagtgggg gtgctggcta tgtccgaagc agccaggacc tgagctgtga cttctgcaat 540
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<210> 19

<211> 1626

<212> DNA

<213> Homo sapiens

<400> 19

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ctcgacacag cagccatttc aaactgggct ttcattccca aaaaaatgc cagctcgat 180
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cagattccca ggcaagagct aaggaagctg tggccaaatg catcccaagc cattagcata 420
gctttcccaa ctttggggc tatcctgaga gaagcccact tgcaaatgt gagtcttccc 480
agacaggtaa atggtctggt gctatcagtg gtttaccag aaagggtgca agaaatcata 540
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aatgtgtggt ttatcatagg ctctcacttt aacattaagg cccaggacta caacatgtgt 960

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attatggatc acaagataag agatgctttg agatgagga tgtcttcact gaaggggaaa	1560
tcgagggcag ctgagaatgc atcacttaggc ccaaccaatg gatctaaattt aatgaatcgt	1620
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<210> 20

<211> 828

<212> DNA

<213> Homo sapiens

<400> 20

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gaccttggaaag ggaaggtcac agccaccacc ttctccctgg agcagcccg cgctgtcttc	180
gatgggcttg ccagcgccag cgataaccgtc tggctcgatgg tggccttcag caatgcctcc	240
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gatggccact acatgacgct gcccctgtct ccggaccaggc tgccctgtgg cgacccatg	360
gcgggcagcg gagggcccccc cgtgctgcgg gtggccatg accacggctg ccaccaggcag	420
cccttctgca acgcgcctt ccctggccct ggaccctatc gggtaagtt ctcctgtatg	480
gacaccaggc gtcacccag ggctgagacc aagtggtcag accccatcac tctccaccaa	540
ggaaagaccc ccggatccat cgacacctgg ccagggccgc gaagtggcag catgatcg	600
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accatgcgct tctccagcct gtggtggccc gaggaggccc cgaggacgct gcggatcgcc 720
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<210> 21
<211> 1308
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76) ... (777)

<400> 21

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Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu	
1 5 10	
ctt ctt gga tct atg tat ggt tat gac aag aaa gga aac aat gca aac	159
Leu Leu Gly Ser Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn	
15 20 25	
cct gaa gct aat atg aat att agc cag att att tct tac tgg ggt tat	207
Pro Glu Ala Asn Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr	
30 35 40	
cct tat gaa gag tat gat gtt aca aca aaa gat ggt tat atc ctt gga	255
Pro Tyr Glu Glu Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly	
45 50 55 60	
att tat agg att cca cat gga aga gga tgc cca ggg agg aca gct cca	303
Ile Tyr Arg Ile Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro	
65 70 75	
aag cct gct gtg tat ttg cag cat ggc tta att gca tct gcc agt aac	351

Lys Pro Ala Val Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn
 80 85 90
 tgg att tgc aac ctg ccc aac aac agt ttg gct ttc ctt ctg gca gat 399
 Trp Ile Cys Asn Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp
 95 100 105
 agt ggt tat gac gtg ttg ggg aac agc cga gga aac act ttg tcc 447
 Ser Gly Tyr Asp Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser
 110 115 120
 aga aaa cac ctt aaa ttg tca ccg aaa tca cca gaa tac ttg gcc ttc 495
 Arg Lys His Leu Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe
 125 130 135 140
 agt ttg gat gag atg gct aaa tat gac ctt cca gcc aca atc aat ttt 543
 Ser Leu Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe
 145 150 155
 atc ata gag aaa act gga cag aag cga ctc tac tac gtg ggc cac tca 591
 Ile Ile Glu Lys Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser
 160 165 170
 caa ggc acc acc ata gct ttt ata gca ttt tct aca aac cca gaa ctg 639
 Gln Gly Thr Thr Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu
 175 180 185
 gct aaa aag att aag ata ttt ttt gca ctg gct cca gtt gtc aca gtt 687
 Ala Lys Lys Ile Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val
 190 195 200
 aaa tac acc caa agt cct atg aaa aaa cta aca acc ctt tcc agg cga 735
 Lys Tyr Thr Gln Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg
 205 210 215 220
 gta gtt aag gta tgt gac ttc cca agt ttt aat ctg aaa taacta 780
 Val Val Lys Val Cys Asp Phe Pro Ser Phe Asn Leu Lys
 225 230
 aaagttagctc tatttccatt gattcaaca gaagaccaat gacatTTTAC aaACTTCTGA 840
 gaaaataata ggtattcaag atatccatgt aagttcactg atgatgtatg caatcttatt 900

agcagagtgc agggaaactcc ccctgttgc aatctgcctt actttcttca tctatgtcta 960
gaaacgtgtc tgctgcgcca ttcccaacc acagatagag agaacttatt tgattgattg 1020
gttttgtgaa ttttagtagat tgaatttttc tagtgatccc taattttta gggcagtgg 1080
tggttgagtt cacagcatgg aatcagatgg tgtgtgttg aatgttattt ctatgattt 1140
caagctgggt aaatttggc aagaccttaa gttctcttca tctgtaatgt ggggataata 1200
atagttctta ctcataaggc taccctgagg actaagtaaa ttaatacagc atatcctcta 1260
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<210> 22

<211> 1272

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60)...(881)

<400> 22

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atg agg ggc tct cag gag gtg ctg ctg atg tgg ctt ctg gtg ttg gca 107
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
/ 1 5 10 15
gtg ggc ggc aca gag cac gcc tac cgg ccc ggc cgt agg gtg tgt gct 155
Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
20 25 30
gtc cgg gct cac ggg gac cct gtc tcc gag tcg ttc gtg cag cgt gtg 203
Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
35 40 45
tac cag ccc ttc ctc acc acc tgc gac ggg cac cgg gcc tgc agc acc 251
Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
50 55 60

tac	cga	acc	atc	tat	agg	acc	gcc	tac	cgc	cgc	agc	cct	ggg	ctg	gcc	299
Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	Ser	Pro	Gly	Leu	Ala	
65				70				75				80				
cct	gcc	agg	cct	cgc	tac	gcg	tgc	tgc	ccc	ggc	tgg	aag	agg	acc	agc	347
Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	Gly	Trp	Lys	Arg	Thr	Ser	
					85				90			95				
ggg	ctt	cct	ggg	gcc	tgt	gga	gca	gca	ata	tgc	cag	ccg	cca	tgc	cgg	395
Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	Ile	Cys	Gln	Pro	Pro	Cys	Arg	
					100				105			110				
aac	gga	ggg	agc	tgt	gtc	cag	cct	ggc	cgc	tgc	cgc	tgc	cct	gca	gga	443
Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	
					115				120			125				
tgg	cgg	ggt	gac	act	tgc	cag	tca	gat	gtg	gat	gaa	tgc	agt	gct	agg	491
Trp	Arg	Gly	Asp	Thr	Cys	Gln	Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	
					130				135			140				
agg	ggc	ggc	tgt	ccc	cag	cgc	tgc	gtc	aac	acc	gcc	ggc	agt	tac	tgg	539
Arg	Gly	Gly	Cys	Pro	Gln	Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	
					145				150			155			160	
tgc	cag	tgt	tgg	gag	ggg	cac	agc	ctg	tct	gca	gac	ggt	aca	ctc	tgt	587
Cys	Gln	Cys	Trp	Glu	Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	
					165				170			175				
gtg	ccc	aag	gga	ggg	ccc	ccc	agg	gtg	gcc	ccc	aac	ccg	aca	gga	gtg	635
Val	Pro	Lys	Gly	Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	
					180				185			190				
gac	agt	gca	atg	aag	gaa	gaa	gtg	cag	agg	ctg	cag	tcc	agg	gtg	gac	683
Asp	Ser	Ala	Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	
					195				200			205				
ctg	ctg	gag	gag	aag	ctg	cag	ctg	gtg	ctg	gcc	cca	ctg	cac	agc	ctg	731
Leu	Leu	Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	
					210				215			220				

gcc tcg cag gca ctg gag cat ggg ctc ccg gac ccc ggc agc ctc ctg 779
Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
225 230 235 240
gtg cac tcc ttc cag cag ctc ggc cgc atc gac tcc ctg agc gag cag 827
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln
245 250 255
att tcc ttc ctg gag gag cag ctg ggg tcc tgc tcc tgc aag aaa gac 875
Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
260 265 270
tcg tgactgccca gcgcgccagg ctggactgag cccctcacgc cgccctgcag cc 930
Ser
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<210> 23

<211> 2083

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (188)...(1036)

<400> 23

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tccccctccct	tccccggccc	cggctctggc	cccgccccat	tcgctgttgg	gtcttctgct	180											
agggagg	atg	tcg	ggt	tcg	ctg	ccc	agc	gcc	ctg	gcc	ctc	tcg	ctg	229			
	Met	Ser	Gly	Ser	Ser	Leu	Pro	Ser	Ala	Leu	Ala	Leu	Ser	Leu			
1		5				10											
ttg	ctg	gtc	tct	ggc	tcc	ctc	ctc	cca	ggg	cca	ggc	gcc	gct	cag	aac	277	
Leu	Leu	Val	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Pro	Gly	Ala	Ala	Gln	Asn		
15		20				25						30					
gag	cca	agg	att	gtc	acc	agt	gaa	gag	gtc	att	att	cga	gac	agc	cct	325	
Glu	Pro	Arg	Ile	Val	Thr	Ser	Glu	Glu	Val	Ile	Ile	Arg	Asp	Ser	Pro		
	35				40							45					
gtt	ctc	cct	gtc	acc	ctg	cag	tgt	aat	aac	ctc	acc	tcc	agc	tct	cac	acc	373
Val	Leu	Pro	Val	Thr	Leu	Gln	Cys	Asn	Leu	Thr	Ser	Ser	Ser	His	Thr		
	50				55						60						
ctt	aca	taa	agc	tac	tgg	aca	aag	aat	ggg	gtg	gaa	ctg	agt	gcc	act	421	
Leu	Thr	Tyr	Ser	Tyr	Trp	Thr	Lys	Asn	Gly	Val	Glu	Leu	Ser	Ala	Thr		
	65				70						75						
cgt	aag	aat	gcc	agc	aac	atg	gag	tac	agg	atc	aat	aag	ccg	aga	gct	469	
Arg	Lys	Asn	Ala	Ser	Asn	Met	Glu	Tyr	Arg	Ile	Asn	Lys	Pro	Arg	Ala		
	80				85						90						
gag	gat	tca	ggc	gaa	tac	cac	tgc	gta	tat	cac	ttt	gtc	agc	gct	cct	517	
Glu	Asp	Ser	Gly	Glu	Tyr	His	Cys	Val	Tyr	His	Phe	Val	Ser	Ala	Pro		
	95				100						105			110			
aaa	gca	aac	gcc	acc	att	gaa	gtg	aaa	gcc	gct	cct	gac	atc	act	ggc	565	
Lys	Ala	Asn	Ala	Thr	Ile	Glu	Val	Lys	Ala	Ala	Pro	Asp	Ile	Thr	Gly		
	115				120						125						
cat	aaa	cg	agt	gag	aac	aag	aat	gaa	ggg	cag	gat	gcc	act	atg	tat	613	
His	Lys	Arg	Ser	Glu	Asn	Lys	Asn	Glu	Gly	Gln	Asp	Ala	Thr	Met	Tyr		
	130				135						140						
tgc	aag	tca	gtt	ggc	tac	ccc	cac	cca	gac	tgg	ata	tgg	cgc	aag	aag	661	
Cys	Lys	Ser	Val	Gly	Tyr	Pro	His	Pro	Asp	Trp	Ile	Trp	Arg	Lys	Lys		

145	150	155	
gag aac ggg atg ccc atg gac att gtc aat acc tct ggc cgc ttc ttc			709
Glu Asn Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe			
160	165	170	
atc atc aac aag gaa aat tac act gag ttg aac att gtg aac ctg cag			757
Ile Ile Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln			
175	180	185	190
atc acg gaa gac cct ggc gag tat gaa tgt aat gcc acc aac gcc att			805
Ile Thr Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile			
195	200	205	
ggc tcc gcc tct gtt gtc act gtc ctc agg gtg cgg agc cac ctg gcc			853
Gly Ser Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala			
210	215	220	
cca ctc tgg cct ttc ttg gga att ctg gct gaa att atc atc ctt gtg			901
Pro Leu Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val			
225	230	235	
gtg atc att gtt gtg tat gag aag agg aag agg cca gat gag gtt cct			949
Val Ile Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro			
240	245	250	
gac gat gat gaa cca gct gga cca atg aaa acc aac tct acc aac aat			997
Asp Asp Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn			
255	260	265	270
cac aaa gat aaa aac ttg cgc cag aga aac aca aat taagtac			1040
His Lys Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn			
275	280		
tgcttacaat atcttttaggt tcctgaaact ggtggcaaca tgacctgcta aaattttctg			1100
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catgccttat ttagcctctc ctgtaagggt gatctagcca ggtacatttt aaacaatgct			1220
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tctAGTgata cactTTTgta aagtacAGCA aaACCTACAG ATATATAcAG tatataAAATA 1460
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gttTCATTT taAGCTGCTG ATATTCAATT CTTATTGTT gttGTcAGAT gagGAATTG 1580
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TCCTTTGCA CTGATGTGTT GAACCTTATT CTTGTACATT CATTCAATCA AGGCAAACCT 1820
TTATAATTAA TCTTTGTTT CCAATGACCT TGAAATGTTA TAGCATGGTA ATATTCTATG 1880
CAACTATAGT TATACTTTT GGTTTGACAC TGTATTTT cacATTGATT TACTGGTTGA 1940
TGATAGATT TATAACCTAA CGGTTCTCAT GCGGTGCGTA ATTGTAGATG CATGTACTTG 2000
TGTGTTTGT GTAATTATTG AAGTGCAATG ATGTATAAAA AAGTGGATTc ACCTGTTTT 2060
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<210> 24

<211> 1260

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147) ... (863)

<400> 24

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ggGACGGGGA GCCCCGGGG GCCCCGCCAC TGCCGCCGTC CGCCGTCACC TACCCGGACT 120
ggATCGGCCA gagTTACTCC gagGTG ATG AGC CTC AAC GAG CAC TCC ATG 170

Met Ser Leu Asn Glu His Ser Met

1

5

cAG GCG CTG TCC TGG CGC AAG CTC TAC TTG AGC CGC GCC AAG CTT AAA 218

Gln Ala Leu Ser Trp Arg Lys Leu Tyr Leu Ser Arg Ala Lys Leu Lys
 10 15 20
 gcc tcc agc cgg acc tcg gct ctg ctc tcc ggc ttc gcc atg gtg gca 266
 Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser Gly Phe Ala Met Val Ala
 25 30 35 40
 atg gtg gag gtg cag ctg gac gct gac cac gac tac cca ccg ggg ctg 314
 Met Val Glu Val Gln Leu Asp Ala Asp His Asp Tyr Pro Pro Gly Leu
 45 50 55
 ctc atc gcc ttc agt gcc tgc acc aca gtg ctg gtg gct gtg cac ctg 362
 Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala Val His Leu
 60 65 70
 ttt gcg ctc atg atc agc acc tgc atc ctg ccc aac atc gag gcg gtg 410
 Phe Ala Leu Met Ile Ser Thr Cys Ile Leu Pro Asn Ile Glu Ala Val
 75 80 85
 agc aac gtg cac aat ctc aac tcg gtc aag gag tcc ccc cat gag cgc 458
 Ser Asn Val His Asn Leu Asn Ser Val Lys Glu Ser Pro His Glu Arg
 90 95 100
 atg cac cgc cac atc gag ctg gcc tgg gcc ttc tcc acc gtc atc ggc 506
 Met His Arg His Ile Glu Leu Ala Trp Ala Phe Ser Thr Val Ile Gly
 105 110 115 120
 acg ctg ctc ttc cta gct gag gtg gtg ctg ctc tgc tgg gtc aag ttc 554
 Thr Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp Val Lys Phe
 125 130 135
 ttg ccc ctc aag aag cag cca ggc cag cca agg ccc acc agc aag ccc 602
 Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg Pro Thr Ser Lys Pro
 140 145 150
 ccc gcc agt ggc gca gca gca aac gtc agc acc agc ggc atc acc ccg 650
 Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr Ser Gly Ile Thr Pro
 155 160 165
 ggc cag gca get gcc atc gcc tcg acc acc atc atg gtg ccc ttc ggc 698

Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile Met Val Pro Phe Gly
 170 175 180
 ctg atc ttt atc gtc ttc gcc gtc cac ttc tac cgc tca ctg gtt agc 746
 Leu Ile Phe Ile Val Phe Ala Val His Phe Tyr Arg Ser Leu Val Ser
 185 190 195 200
 cat aag acc gac cga cag ttc cag gag ctc aac gag ctg gcg gag ttt 794
 His Lys Thr Asp Arg Gln Phe Glu Leu Asn Glu Leu Ala Glu Phe
 205 210 215
 gcc cgc tta cag gac cag ctg gac cac aga ggg gac cac ccc ctg acg 842
 Ala Arg Leu Gln Asp Gln Leu Asp His Arg Gly Asp His Pro Leu Thr
 220 225 230
 ccc ggc agc cac tat gcc taggccccatg tggctggc ccttccagtg 890
 Pro Gly Ser His Tyr Ala
 235
 ctggccctt acggcccttcc cttgacctt gtcctgcccc agcctcacgg acagcctgcg 950
 cagggggctg ggcttcagca aggggcagag cgtggaggga agaggatttt tataagagaa 1010
 atttctgcac ttgaaactg tcctctaaga gaataagcat ttccctgttct tccagctcca 1070
 ggtccacctc ctgttggag gcgggtgggg gccaaagtgg ggccacacac tcgctgtgtc 1130
 ccctctccctc ccctgtgccca gtgccacctg ggtgcctcct cctgtcctgt ccgtctcaac 1190
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<210> 25

<211> 1720

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (282)...(1400)

<400> 25

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aggaggtctc tgctgctgat gaagctgtga ccaa(ac)cac ccaacccttg gcagccatct	120
gtccctgcag ccatagccca cattcccatg acctccctct gcttgtttg ggaccatgtc	180
tgtacagcct ctaggccccca gccccggagg tgaatgccat gccatgattc tggtgtgctc	240
catggcatcc ccagcctagc tcccaatccc actttggcac g atg tta gcc aac	293
Met Leu Ala Asn	
1	
agc tcc tca acc aac agt tct gtt ctc ccg tgt cct gac tac cga cct	341
Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro Asp Tyr Arg Pro	
5 10 15 20	
acc cac cgc ctg cac ttg gtg gtc tac agc ttg gtg ctg gct gcc ggg	389
Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val Leu Ala Ala Gly	
25 30 35	
ctc ccc ctc aac gcg cta gcc ctc tgg gtc ttc ctg cgc gcg ctg cgc	437
Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu Arg Ala Leu Arg	
40 45 50	
gtg cac tcg gtg gtg agc gtg tac atg tgt aac ctg gcg gcc agc gac	485
Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu Ala Ala Ser Asp	
55 60 65	
ctg ctc ttc acc ctc tcg ccc gtt cgt ctc tcc tac tac gca ctg	533
Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser Tyr Tyr Ala Leu	
70 75 80	
cac cac tgg ccc ttc ccc gac ctc ctg tgc cag acg acg ggc gcc atc	581
His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr Thr Gly Ala Ile	
85 90 95 100	
ttc cag atg aac atg tac ggc agc tgc atc ttc ctg atg ctc atc aac	629
Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu Met Leu Ile Asn	
105 110 115	
gtg gac cgc tac gcc gcc atc gtg cac ccg ctg cga ctg cgc cac ctg	677

Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg Leu Arg His Leu			
120	125	130	
cgg cgg ccc cgc gtg gcg cgg ctg ctc tgc ctg ggc gtg tgg gcg ctc			725
Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly Val Trp Ala Leu			
135	140	145	
atc ctg gtg ttt gcc gtg ccc gcc gac cgc gtg cac agg ccc tcg cgt			773
Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His Arg Pro Ser Arg			
150	155	160	
tgc cgc tac cgg gac ctc gag gtg cgc cta tgc ttc gag agc ttc agc			821
Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe Glu Ser Phe Ser			
165	170	175	180
gac gag ctg tgg aaa ggc agg ctg ctg ccc ctc gtg ctg ctg gcc gag			869
Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val Leu Leu Ala Glu			
185	190	195	
gcg ctg ggc ttc ctg ccc ctg gcg gcg gtg gtc tac tcg tcg ggc			917
Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val Tyr Ser Ser Gly			
200	205	210	
cga gtc ttc tgg acg ctg gcg cgc ccc gac gcc acg cag agc cag cgg			965
Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr Gln Ser Gln Arg			
215	220	225	
cg ^g cgg aag acc gtg cgc ctc ctg ctg gct aac ctc gtc atc ttc ctg			1013
Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu Val Ile Phe Leu			
230	235	240	
ctg tgc ttc gtg ccc tac aac agc acg ctg gcg gtc tac ggg ctg ctg			1061
Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val Tyr Gly Leu Leu			
245	250	255	260
cg ^g agc aag ctg gtg gcg gcc agc gtg cct gcc cgc gat cgc gtg cgc			1109
Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg Asp Arg Val Arg			
265	270	275	
ggg gtg ctg atg gtg atg gtg ctg ctg gcc ggc gcc aac tgc gtg ctg			1157

Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala Asn Cys Val Leu
 280 285 290
 gac ccg ctg gtg tac tac ttt agc gcc gag ggc ttc cgc aac acc ctg 1205
 Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe Arg Asn Thr Leu
 295 300 305
 cgc ggc ctg ggc act ccg cac cgg gcc agg acc tcg gcc acc aac ggg 1253
 Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser Ala Thr Asn Gly
 310 315 320
 acg cgg gcg gcg ctc gcg caa tcc gaa agg tcc gcc gtc acc acc gac 1301
 Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala Val Thr Thr Asp
 325 330 335 340
 gcc acc agg ccg gat gcc gcc agt cag ggg ctg ctc cga ccc tcc gac 1349
 Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu Arg Pro Ser Asp
 345 350 355
 tcc cac tct ctg tct tcc ttc aca cag tgt ccc cag gat tcc gcc ctc 1397
 Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln Asp Ser Ala Leu
 360 365 370
 tga acacacatgc cattgcgtcg tccgtgccccg actcccaacg cctctcggttc 1450
 tggaggctt acagggtgta cacacaagaa ggtggctgg gcacttggac ctttgggtgg 1510
 caattccagc tttagcaacgc agaagagtac aaagtgtgga agccagggcc cagggaaaggc 1570
 agtgctgctg gaaatggctt cttaaactg tgagcacgca gagcacccct tctccagcgg 1630
 tgggaagtga tgcagagagc ccacccgtgc agagggcaga agaggacgaa atgccttgg 1690
 gtggcaggg cattaaactg ctaaaagctg 1720

<210> 26

<211> 2237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25) . . . (465)

<400> 26

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Met Trp Lys Leu Trp Arg Ala Glu Glu
1 5
ggc gcg gcg gcg ctc ggc ggc gcg ctc ttc ctg ctg ctc ttc gcg cta
Gly Ala Ala Ala Leu Gly Gly Ala Leu Phe Leu Leu Leu Phe Ala Leu
10 15 20 25
ggg gtc cgc cag ctg ctg aag cag agg cgg ccg atg ggc ttc ccc ccc
Gly Val Arg Gln Leu Leu Lys Gln Arg Arg Pro Met Gly Phe Pro Pro
30 35 40
ggg ccg ccg ggg ctg cca ttt atc ggc aac atc tat tcc ctg gca gcc
Gly Pro Pro Gly Leu Pro Phe Ile Gly Asn Ile Tyr Ser Leu Ala Ala
45 50 55
tca tcc gag ctt ccc cat gtc tac atg aga aag cag agc cag gtg tac
Ser Ser Glu Leu Pro His Val Tyr Met Arg Lys Gln Ser Gln Val Tyr
60 65 70
gga gag gta cag ccc cga cgg gcc ccg ggc agg gag ggc cgc cag gct
Gly Glu Val Gln Pro Arg Arg Ala Pro Gly Arg Glu Gly Arg Gln Ala
75 80 85
ggc ccg ggc tgg cca ggg cct tcc tgg ttg gac tta tgg ccg ccc ctg
Gly Pro Gly Trp Pro Gly Pro Ser Trp Leu Asp Leu Trp Pro Pro Leu
90 95 100 105
ggc cga cta gtc ggg acc tct ccg tgt gcc ggc tgc cct ttg agg gac
Gly Arg Leu Val Gly Thr Ser Pro Cys Ala Gly Cys Pro Leu Arg Asp
110 115 120
acc cgc ttc ccg ggt ctg gaa ggg aga agt cct cga cgc cgt gcc ccc
Thr Arg Phe Pro Gly Leu Glu Gly Arg Ser Pro Arg Arg Arg Ala Pro
125 130 135

ttg cag ggg gag ccc cgc ccc tgc cg ^g tgacccactc cggggccga	480
Leu Gln Gly Glu Pro Arg Pro Cys Arg	
140	145
ggctccgagg cgatccagtc ctgatttcc cgctaccgct cgagctcttg ctcc ^t cgcc	540
tgcgcgttt ggctcgccag ccgcgcgc ac ^t cagg ^t tc cagggtggac gcatgcctc	600
agg ^t gcgggc gtcttgcgag tcggcctcgc agctctgtgg aagctgcacg cggcttgtcg	660
gaaaatcaag gcgttctgag ttctagatgg ttaatagcag gttttcggt gtctgcagtc	720
gacgaacgac tgg ^t taggc gtttgc ^t tg ^t agaatggaga atgcagggga acgccc ^t ga	780
ctgagaagcg ggccctggga aacgattgt ^t aacgcgtgaa tgaattgat ^t actaaaatcc	840
gctgcggggg tcctacagcg cagatggtaa tgccgttctg actggctggg aacggcacct	900
tagcagatac ttaaaaggcg ctttctgtgt gccactgtca ctgccaactt ggtgactcat	960
ttaaaactca taaccagccg gtgagg ^t tcgg tacttcgctc ctcc ^t cattc tgcggagggg	1020
aaagcagcac ggaaatgccc tgtgactggc agcggaaaag gcgaccac ^t g cttgttatc	1080
ttcagtttag atcttggagg catatcaact gtgg ^t tctaa atggctatga tgttagtaaag	1140
gaatgcctt ^t ttc ^t catcaaag cgaaat ^t ttt gcagacagac catgccttcc tttattcatg	1200
aagatgacaa aaatggagg cttactcaat tccagatatg gccgaggatg gtttgatcac	1260
agacgattag ctgtaaacag tttcgat ^t tttggatatg gccaaaagtc tttgaatct	1320
aaaatcttgg aagaaaccaa attttcaat gatgctattg aaacatacaa agtagac ^t t	1380
tttgacttta aacagttaat aacgaatgct gtttcaaaca taaccaatct gatcatttt	1440
ggagaacgat tcacttatga agacaccgat tttcagcaca tgattgagtt atttagt ^t gaa	1500
aatgtggaac tagctgccag tgcctcagtc ttcttgata atgccttcc atggattggc	1560
atcctgcctt ttggaaaaca tcaacagctg tttagaaatg cagctgttagt ctatgatttt	1620
ctctccagac tcattgaaaa agcttcagtc aacagaaaagc ct ^t cagctacc tcagcatttt	1680
gttgatgctt atttagatga gatggatcaa ggtaaaaatg acccatcatc tactttctcc	1740
aaagaaaaacc taat ^t ttctc agtgggtgaa ctcatcattg ctggaactga aactacaacc	1800
aatgtgctac ggtgggc ^t at tctttcatg gccctttatc ctaatattca agtactggag	1860
agacc ^t cagaa gtgttccatc ctgagc ^t att tctggacagc agtggatatt ttgccaagaa	1920
ggaagctt ^t g gttcctttt ccctaggaag aagacattgt ctggagaac acttggctcg	1980
gatggaaatg ttcttgc ^t ttt ttacagcatt gcttcagagg tt ^t catttgc attttccaca	2040
tgaactagtt ccagatctga agcc ^t caggtt aggcatgaca ttgcagcccc aaccctac ^t t	2100

catctgtgct gaaagacgct gaaactgcct gggatgttt cggacaacaag aatgttatatt 2160
tgccttatcc ctgaaccttg tttaatcaaa tcaatgtgtg tattagaata aaagtacacag 2220
catcaaaaag ccaaatg 2237

<210> 27

<211> 1687

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (268) ... (1176)

<400> 27

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aatcttggaaag ggcgggtgaaa aacctacgtc ctggccctcgc ccggcctctc cattcgtccc 180
ccgggttagag aggtgccccgg ctcccaccccc ttcccagccc cagcccttggaa gacagcagcc 240
ccttagactac tgagggacacag cgacacgc atg aag gct ccg ggt cgg ctc gtg 291

Met Lys Ala Pro Gly Arg Leu Val

1 5

ctc atc atc ctg tgc tcc gtg gtc ttc tct gcc gtc tac atc ctc ctg 339

Leu Ile Ile Leu Cys Ser Val Val Phe Ser Ala Val Tyr Ile Leu Leu

10 15 20

tgc tgc tgg gcc ggc ctg ccc ctc tgc ctg gcc acc tgc ctg gac cac 387

Cys Cys Trp Ala Gly Leu Pro Leu Cys Leu Ala Thr Cys Leu Asp His

25 30 35 40

cac ttc ccc aca ggc tcc agg ccc act gtg ccg gga ccc ctg cac ttc 435

His Phe Pro Thr Gly Ser Arg Pro Thr Val Pro Gly Pro Leu His Phe

45 50 55

agt gga tat agc agt gtg cca gat ggg aag ccg ctg gtc cgc gag ccc			483
Ser Gly Tyr Ser Ser Val Pro Asp Gly Lys Pro Leu Val Arg Glu Pro			
60	65	70	
tgc cgc agc tgt gcc gtg gtg tcc agc tcc ggc caa atg ctg ggc tca			531
Cys Arg Ser Cys Ala Val Val Ser Ser Ser Gly Gln Met Leu Gly Ser			
75	80	85	
ggc ctg ggt gct gag atc gac agt gcc gag tgc gtg ttc cgc atg aac			579
Gly Leu Gly Ala Glu Ile Asp Ser Ala Glu Cys Val Phe Arg Met Asn			
90	95	100	
cag gcg ccc acc gtg ggc ttt gag gcg gat gtg ggc cag cgc agc acc			627
Gln Ala Pro Thr Val Gly Phe Glu Ala Asp Val Gly Gln Arg Ser Thr			
105	110	115	120
ctg cgt gtc gtc tca cac aca agc gtg ccg ctg ctg ctg cgc aac tat			675
Leu Arg Val Val Ser His Thr Ser Val Pro Leu Leu Arg Asn Tyr			
125	130	135	
tca cac tac ttc cag aag gcc cga gac acg ctc tac atg gtg tgg ggc			723
Ser His Tyr Phe Gln Lys Ala Arg Asp Thr Leu Tyr Met Val Trp Gly			
140	145	150	
cag ggc agg cac atg gac cgg gtg ctc ggc ggc cgc acc tac cgc acg			771
Gln Gly Arg His Met Asp Arg Val Leu Gly Gly Arg Thr Tyr Arg Thr			
155	160	165	
ctg ctg cag ctc acc agg atg tac ccc ggc ctg cag gtg tac acc ttc			819
Leu Leu Gln Leu Thr Arg Met Tyr Pro Gly Leu Gln Val Tyr Thr Phe			
170	175	180	
acg gag cgc atg atg gcc tac tgc gac cag atc ttc cag gac gag acg			867
Thr Glu Arg Met Met Ala Tyr Cys Asp Gln Ile Phe Gln Asp Glu Thr			
185	190	195	200
ggc aag aac cgg agg cag tcg ggc tcc ttc ctc agc acc ggc tgg ttc			915
Gly Lys Asn Arg Arg Gln Ser Gly Ser Phe Leu Ser Thr Gly Trp Phe			
205	210	215	

acc atg atc ctc gcg ctg gag ctg tgt gag gag atc gtg gtc tat ggg		963	
Thr Met Ile Leu Ala Leu Glu Leu Cys Glu Glu Ile Val Val Tyr Gly			
220	225	230	
atg gtc agc gac agc tac tgc agg gag aag agc cac ccc tca gtg cct		1011	
Met Val Ser Asp Ser Tyr Cys Arg Glu Lys Ser His Pro Ser Val Pro			
235	240	245	
tac cac tac ttt gag aag ggc cg ^g cta gat gag tgt cag atg tac ctg		1059	
Tyr His Tyr Phe Glu Lys Gly Arg Leu Asp Glu Cys Gln Met Tyr Leu			
250	255	260	
gca cac gag cag gcg ccc cga agc gcc cac cgc ttc atc act gag aag		1107	
Ala His Glu Gln Ala Pro Arg Ser Ala His Arg Phe Ile Thr Glu Lys			
265	270	275	280
g ^c g gtc ttc tcc cgc tgg gcc aag aag agg ccc atc gtg ttc gcc cat		1155	
Ala Val Phe Ser Arg Trp Ala Lys Lys Arg Pro Ile Val Phe Ala His			
285	290	295	
ccg tcc tgg agg act gag tagcttccgt cgtcctgcc ^a gcccgc ^a atgc cg ^t tg ^c g		1210	
Pro Ser Trp Arg Thr Glu			
300			
aggcctccgg gatgtcccat cccaa ^g ccat cacactccac aaaaacattt aatttatgg ^a		1270	
tcctgcctcc tgccacgtgc tgggtggacc taaggttcc ^t tcccgcccc ^a ttctggcgac		1330	
acttggagcc atctcaggcc tc ^a tgacttg aaggggagtg gaggggggag ccgtgtctcc		1390	
cccctccact ccctgagtaa ttcatggcat ttgggggctc accccac ^t tc caggtctgtc		1450	
aagtggc ^t tt tgccctggg gctgatggcc cccaa ^t tc ac cagcatcatg acctt ^t tgcc		1510	
agtccctggc ^t ctc ^t ccccc agccgcccc ^t accac ^t ttt ggtgccacac ttctcaggct		1570	
ggccgc ^t ctg gttggggcag ccgagagc ^t ggggttcatt ggtgaagggg ccttggagtt		1630	
gtgactgccc ^t gggccgtatc aggaacgtac gggtaaacgt gtgtttctg gatgctg		1687	

<210> 28

<211> 963

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (246) ... (830)

<400> 28

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aggactctat ataaatcgct gtgggctcac cacctctaag gaggagcact gactgaagac	120
agaaaaattg atgaactgaa gaagacatgg tccattatgc cttacaaact tacacagtgc	180
tttggaaatt ccaaagtact cagtggagag aggtgttca ggagccgtag agccagatcg	240
tcatc atg tct gca ttg tgg ctg ctg ggc ctc ctt gcc ctg atg	287
Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met	
1 5 10	
gac ttg tct gaa agc agc aac tgg gga tgc tat gga aac atc caa agc	335
Asp Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser	
15 20 25 30	
ctg gac acc cct gga gca tct tgt ggg att gga aga cgt cac ggc ctg	383
Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu	
35 40 45	
aac tac tgt gga gtt cgt gct tct gaa agg ctg gct gaa ata gac atg	431
Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met	
50 55 60	
cca tac ctc ctg aaa tat caa ccc atg atg caa acc att ggc caa aag	479
Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys	
65 70 75	
tac tgc atg gat cct gcc gtg atc gct ggt gtc ttg tcc agg aag tct	527
Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser	
80 85 90	
ccc ggt gac aaa att ctg gtc aac atg ggc gat agg act agc atg gtg	575

Pro Gly Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val
 95 100 105 110
 cag gac cct ggc tct caa gct ccc aca tcc tgg att agt gag tct cag 623
 Gln Asp Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln
 115 120 125
 gtt tcc cag aca act gaa gtt ctg act act aga atc aaa gaa atc cag 671
 Val Ser Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln
 130 135 140
 agg agg ttt cca acc tgg acc cct gac cag tac ctg aga ggt gga ctc 719
 Arg Arg Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu
 145 150 155
 tgt gcc tac agt ggg ggt gct ggc tat gtc cga agc agc cag gac ctg 767
 Cys Ala Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu
 160 165 170
 agc tgt gac ttc tgc aat gat gtc ctt gca cga gcc aag tac ctc aag 815
 Ser Cys Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys
 175 180 185 190
 aga cat ggc ttc taacatctca gatgaaaccc aagaccatga tcacatatgc agc 870
 Arg His Gly Phe

 ctcaaatgtt acacagataa aactagccaa gggcacctgt aactggaat ctgagttga 930
 cctaaaagtc attaaaataa catgaatcac att 963

<210> 29

<211> 2667

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (229) ... (1857)

<400> 29

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gatggtgagg	catcatgcta	gggagctgag	ctctgac	cctgctgggt	gattctccac	180
ctctggctg	ctagatctac	ttcctggatg	ccgtgaagat	cctcatgt	atg aaa	234
					Met Lys	
					1	
atg aag tcc cag gca acc atg att tgc tgc tta gtg ttc ttt ctg tcc						282
Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe Leu Ser						
5	10	15				
aca gaa tgt tcc cac tat aga tcc aag att cac cta aaa agc tat agt						330
Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser Tyr Ser						
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gaa gtg gcc aac cac atc ctc gac aca gca gcc att tca aac tgg gct						378
Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn Trp Ala						
35	40	45			50	
ttc att ccc aac aaa aat gcc agc tcg gat ttg ttg cag tca gtg aat						426
Phe Ile Pro Asn Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn						
55	60	65				
ttg ttt gcc aga caa ctc cac atc cac aat aat tct gag aac att gtg						474
Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn Ile Val						
70	75	80				
aat gaa ctc ttc att cag aca aaa ggg ttt cac atc aac cat aat acc						522
Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His Asn Thr						
85	90	95				
tca gag aaa agc ctc aat ttc tcc atg agc atg aac aat acc aca gaa						570
Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu						
100	105	110				

gat atc tta gga atg gta cag att ccc agg caa gag cta agg aag ctg			618
Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg Lys Leu			
115	120	125	130
tgg cca aat gca tcc caa gcc att agc ata gct ttc cca acc ttg ggg			666
Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr Leu Gly			
135	140	145	
gct atc ctg aga gaa gcc cac ttg caa aat gtg agt ctt ccc aga cag			714
Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro Arg Gln			
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Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu			
165	170	175	
atc ata ctc acc ttc gaa aag atc aat aaa acc cgc aat gcc aga gcc			810
Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala			
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cag tgt gtt ggc tgg cac tcc aag aaa agg aga tgg gat gag aaa gcg			858
Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu Lys Ala			
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tgc caa atg atg ttg gat atc agg aac gaa gtg aaa tgc cgc tgt aac			906
Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg Cys Asn			
215	220	225	
tac acc agt gtg gtg atg tct ttt tcc att ctc atg tcc tcc aaa tcg			954
Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser Lys Ser			
230	235	240	
atg acc gac aaa gtt ctg gac tac atc acc tgc att ggg ctc agc gtc			1002
Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu Ser Val			
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Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr Val Trp			
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Ser	Arg	Val	Val	Val												
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gtg	aatata	gca	gtgtcccttctgact	gccaatgtgtgg	tttatcata	1146										
Val	Asn	Ile	Ala	Val	Ser	Leu	Leu	Thr	Ala	Asn	Val	Trp	Phe	Ile	Ile	
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gtg	aca	tttttc	agc	cac	tttttc	tac	ctc	tct	ctg	tttttc	tgg	atg	1242			
Val	Thr	Phe	Phe	Ser	His	Phe	Phe	Tyr	Leu	Ser	Leu	Phe	Phe	Trp	Met	
	325		330		335											
ctc	ttcaaa	gca	ttgttc	atc	att	tat	gga	ata	ttgttc	gtc	att	ttc	cgt	1290		
Leu	Phe	Lys	Ala	Leu	Leu	Ile	Ile	Tyr	Gly	Ile	Leu	Val	Ile	Phe	Arg	
	340		345		350											
agg	atg	atg	aag	tcc	cga	atg	atg	gtc	att	ggc	ttt	gcc	att	ggc	tat	1338
Arg	Met	Met	Lys	Ser	Arg	Met	Met	Val	Ile	Gly	Phe	Ala	Ile	Gly	Tyr	
	355		360		365		370									
ggg	tgc	ccat	ttg	atc	att	gct	gtc	act	aca	gtt	gct	atc	aca	gag	cca	1386
Gly	Cys	Pro	Leu	Ile	Ile	Ala	Val	Thr	Thr	Val	Ala	Ile	Thr	Glu	Pro	
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gag	aac	ggc	tac	atg	aga	cct	gag	gcc	tgt	tgg	ctt	aac	tgg	gac	aat	1434
Glu	Asn	Gly	Tyr	Met	Arg	Pro	Glu	Ala	Cys	Trp	Leu	Asn	Trp	Asp	Asn	
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Thr	Lys	Ala	Leu	Leu	Ala	Phe	Ala	Ile	Pro	Ala	Phe	Val	Ile	Val	Ala	
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Val	Asn	Leu	Ile	Val	Val	Leu	Val	Val	Ala	Val	Asn	Thr	Gln	Arg	Pro	
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Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met Arg Ile			
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Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly			
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ttt gga ata gcc act ctc ata gaa ggc act tcc ttg acg ttc cat ata			1674
Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe His Ile			
470	475	480	
att ttt gcc ttg ctc aat gct ttc cag ggt ttt ttc atc ctg ctg ttt			1722
Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu Leu Phe			
485	490	495	
gga acc att atg gat cac aag ata aga gat gct ttg agg atg agg atg			1770
Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met Arg Met			
500	505	510	
tct tca ctg aag ggg aaa tcg agg gca gct gag aat gca tca cta ggc			1818
Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser Leu Gly			
515	520	525	530
cca acc aat gga tct aaa tta atg aat cgt caa gga tgaaatgctg ccccat			1870
Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly			
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cagcccgaaag cagccagacc agccctgag cctcccgggt gctggcagct gtc atg 176

Met

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Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu Leu

5

10

15

gcg ttg aac tgt ctc cgg ccc agc ctg agc ctg gag ctg gtg ccc tac 272

Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro Tyr

20

25

30

aca cca cag ata aca gct tgg gac ctg gaa ggg aag gtc aca gcc acc 320

Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala Thr

35

40

45

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Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala Ser			
50	55	60	65
gcc agc gat acc gtc tgg ctc gtg gtg gcc ttc agc aat gcc tcc agg			416
Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser Arg			
70	75	80	
ggc ttc cag aac ccg gag aca ctg gct gac att ccg gcc tcc cca cag			464
Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro Gln			
85	90	95	
ctg ctg acc gat ggc cac tac atg acg ctg ccc ctg tct ccg gac cag			512
Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp Gln			
100	105	110	
ctg ccc tgt ggc gac ccc atg gcg ggc agc gga ggc gcc ccc gtg ctg			560
Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val Leu			
115	120	125	
cgg gtg ggc cat gac cac ggc tgc cac cag cag ccc ttc tgc aac gcg			608
Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn Ala			
130	135	140	145
ccc ctc cct ggc cct gga ccc tat cgg gtg aag ttc ctc ctg atg gac			656
Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met Asp			
150	155	160	
acc agg ggc tca ccc agg gct gag acc aag tgg tca gac ccc atc act			704
Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile Thr			
165	170	175	
ctc cac caa ggg aag acc ccc gga tcc atc gac acc tgg cca ggg cgg			752
Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly Arg			
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Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu Ala			
195	200	205	

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Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe Ser		
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Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly Ser		
230	235	240
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Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu Ala		
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Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro Ser		
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Leu Ser Pro		
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